

GeDiPNet Cluster 607 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See scripts/build_cluster_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:02:22

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Synthesis, secretion, and inactivation of Glucose-dependent Insulinotropic Polypeptide (GIP)	Reactome	1	PAX6	7	6	285.95	3.493e-3	2.829e-2
Synthesis, secretion, and inactivation of Glucagon-like Peptide-1 (GLP-1)	Reactome	1	PAX6	14	6	142.98	6.975e-3	4.528e-2
SUMOylation of transcription factors	Reactome	1	MITF	18	6	111.20	8.961e-3	5.313e-2
Maturity onset diabetes of the young	KEGG	1	PAX6	26	6	76.99	1.292e-2	6.623e-2
Pathways in cancer	KEGG	2	MITF, PTCH2	533	6	7.51	2.618e-2	1.003e-1
Hedgehog signaling pathway	KEGG	1	PTCH2	56	6	35.74	2.766e-2	1.031e-1
Basal cell carcinoma	KEGG	1	PTCH2	63	6	31.77	3.107e-2	1.102e-1
Melanoma	KEGG	1	MITF	73	6	27.42	3.593e-2	1.198e-1
Interferon gamma signaling	Reactome	1	MID1	87	6	23.01	4.269e-2	1.323e-1
Melanogenesis	KEGG	1	MITF	101	6	19.82	4.942e-2	1.439e-1
Mitophagy - animal	KEGG	1	MITF	105	6	19.06	5.133e-2	1.468e-1
Ubiquitin mediated proteolysis	KEGG	1	MID1	142	6	14.10	6.889e-2	1.739e-1
Osteoclast differentiation	KEGG	1	MITF	142	6	14.10	6.889e-2	1.739e-1
Signaling pathways regulating pluripotency of stem cells	KEGG	1	PAX6	144	6	13.90	6.983e-2	1.752e-1
Transcriptional misregulation in cancer	KEGG	1	MITF	198	6	10.11	9.495e-2	2.096e-1